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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/397,846

DATE: 10/01/1999
TIME: 11:56:48

Input Set: I397846.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

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1  <110> APPLICANT: Presnell, Scott R.
2      Taft, David W.
3      Foley, Kevin P.
4  <120> TITLE OF INVENTION: Mammalian Transforming Growth Factor Beta - 9
5  <130> FILE REFERENCE: 98-54
6  <140> CURRENT APPLICATION NUMBER: US/09/397,846
7  <141> CURRENT FILING DATE: 1999-09-17
8  <150> EARLIER APPLICATION NUMBER: 60/100,706
9  <151> EARLIER FILING DATE: 1998-09-17
10 <160> NUMBER OF SEQ ID NOS: 22
11 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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13 <211> LENGTH: 1819
14 <212> TYPE: DNA
15 <213> ORGANISM: Homo sapiens
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17 <221> NAME/KEY: CDS
18 <222> LOCATION: (71)...(676)
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20      cgggcgcggg ggcagggcgg gctcctccgg cgctgagcgt ggcctgtccc      60
21      tcaggtctgg atg ctg gta gcc ggc ttc ctg ctg gcg ctg ccg ccg agc      109
22              Met Leu Val Ala Gly Phe Leu Leu Ala Leu Pro Pro Ser
23              1              5              10
24      tgg gcc gcg ggc gcc ccg agg gcg ggc agg cgc ccc gcg cgg ccg cgg      157
25      Trp Ala Ala Gly Ala Pro Arg Ala Gly Arg Arg Pro Ala Arg Pro Arg
26              15              20              25
27      ggc tgc gcg gac cgg ccg gag gag cta ctg gag cag ctg tac ggg cgc      205
28      Gly Cys Ala Asp Arg Pro Glu Glu Leu Leu Glu Gln Leu Tyr Gly Arg
29      30              35              40              45
30      ctg gcg gcc ggc gtg ctc agt gcc ttc cac cac acg ctg cag ctg ggg      253
31      Leu Ala Ala Gly Val Leu Ser Ala Phe His His Thr Leu Gln Leu Gly
32              50              55              60
33      ccg cgt gag cag gcg cgc aac gcg agc tgc ccg gca ggg ggc agg ccc      301
34      Pro Arg Glu Gln Ala Arg Asn Ala Ser Cys Pro Ala Gly Gly Arg Pro
35              65              70              75
36      gcc gac cgc cgc ttc cgg ccg ccc acc aac ctg cgc agc gtg tgc ccc      349
37      Ala Asp Arg Arg Phe Arg Pro Pro Thr Asn Leu Arg Ser Val Ser Pro
38              80              85              90
39      tgg gcc tac aga atc tcc tac gac ccg gcg agg tac ccc agg tac ctg      397
40      Trp Ala Tyr Arg Ile Ser Tyr Asp Pro Ala Arg Tyr Pro Arg Tyr Leu
41              95              100              105
42      cct gaa gcc tac tgc ctg tgc cgg ggc tgc ctg acc ggg ctg ttc ggc      445
43      Pro Glu Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr Gly Leu Phe Gly
44      110              115              120              125

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45      gag gag gac gtg cgc ttc cgc agc gcc cct gtc tac atg ccc acc gtc      493
46      Glu Glu Asp Val Arg Phe Arg Ser Ala Pro Val Tyr Met Pro Thr Val
47                  130                      135                      140
48      gtc ctg cgc cgc acc ccc gcc tgc gcc ggc ggc cgt tcc gtc tac acc      541
49      Val Leu Arg Arg Thr Pro Ala Cys Ala Gly Gly Arg Ser Val Tyr Thr
50                  145                      150                      155
51      gag gcc tac gtc acc atc ccc gtg ggc tgc acc tgc gtc ccc gag ccg      589
52      Glu Ala Tyr Val Thr Ile Pro Val Gly Cys Thr Cys Val Pro Glu Pro
53                  160                      165                      170
54      gag aag gac gca gac agc atc aac tcc agc atc gac aaa cag ggc gcc      637
55      Glu Lys Asp Ala Asp Ser Ile Asn Ser Ser Ile Asp Lys Gln Gly Ala
56                  175                      180                      185
57      aag ctc ctg ctg ggc ccc aac gac gcg ccc gct ggc ccc tgaggccggt      686
58      Lys Leu Leu Leu Gly Pro Asn Asp Ala Pro Ala Gly Pro
59      190                      195                      200
60      cctgccccgg gaggtctccc cggccccgat cccgaggcgc ccaagctgga gccgcctgga      746
61      gggctcggtc ggcgacctct gaagagagtg caccgagcaa accaagtgcc ggagcaccag      806
62      cgccgccttt ccatggagac tcgtaagcag cttcatctga cacgggaatc cctggcttgc      866
63      ttttagctac aagcaagcag cgtggctgga agctgatggg aaacgaccgc gcacgggcat      926
64      cctgtgtgcg gcccgcattg agggtttggg aaagtccacg gaggctccct gaggagcctc      986
65      tcagatcggc tgctgcgggt gcagggcgtg actcaccgct ggggtgcttg caaagagata      1046
66      gggacgcata tgctttttaa agcaatctaa aaataataat aagtatagcg actatatacc      1106
67      tactttttaa atcaactgtt ttgaatagag gcagagctat tttatattat caaatgagag      1166
68      ctactctgtt acatttctta acatataaac atcgtttttt acttcttctg gtagaatttt      1226
69      ttaaagcata attggaatcc ttggataaat tttgtagctg gtacactctg gcctgggtct      1286
70      ctgaattcag cctgtcaccg atggctgact gatgaaatgg acacgtctca tctgaccac      1346
71      tcttccttcc actgaaggtc ttcacgggcc tccaggtgga ccaaagggat gcacagggcg      1406
72      ctgcgatgcc ccagggccag ctaagagttc caaagatctc agatttggtt ttagtcatga      1466
73      atacataaac agtctcaaac tcgcacaatt ttttccccct tttgaaagcc actggggcca      1526
74      atttgtgggt aagaggtggt gagataagaa gtggaacgtg acatctttgc cagttgtcag      1586
75      aagaatccaa gcaggtattg gcttagttgt aagggtctta ggatcaggcc gaatatgagg      1646
76      acaaagtggg ccacgttagc atctgcagag atcaatctgg aggcttctgt ttctgcattc      1706
77      tgccacgaga gctaggtcct tgatcttttc ttttagattga aagtctgtct ctgaacacaa      1766
78      ttatttgtaa aagttagaag ttctttttta aatcattaaa agaggcttgc tga      1819
79      <210> SEQ ID NO 2
80      <211> LENGTH: 202
81      <212> TYPE: PRT
82      <213> ORGANISM: Homo sapiens
83      <400> SEQUENCE: 2
84      Met Leu Val Ala Gly Phe Leu Leu Ala Leu Pro Pro Ser Trp Ala Ala
85      1                      5                      10                      15
86      Gly Ala Pro Arg Ala Gly Arg Arg Pro Ala Arg Pro Arg Gly Cys Ala
87      20                      25                      30
88      Asp Arg Pro Glu Glu Leu Leu Glu Leu Tyr Gly Arg Leu Ala Ala
89      35                      40                      45
90      Gly Val Leu Ser Ala Phe His Thr Leu Gln Leu Gly Pro Arg Glu
91      50                      55                      60
92      Gln Ala Arg Asn Ala Ser Cys Pro Ala Gly Gly Arg Pro Ala Asp Arg
93      65                      70                      75                      80
94      Arg Phe Arg Pro Pro Thr Asn Leu Arg Ser Val Ser Pro Trp Ala Tyr

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95          85          90          95
96      Arg Ile Ser Tyr Asp Pro Ala Arg Tyr Pro Arg Tyr Leu Pro Glu Ala
97          100          105          110
98      Tyr Cys Leu Cys Arg Gly Cys Leu Thr Gly Leu Phe Gly Glu Glu Asp
99          115          120          125
100     Val Arg Phe Arg Ser Ala Pro Val Tyr Met Pro Thr Val Val Leu Arg
101          130          135          140
102     Arg Thr Pro Ala Cys Ala Gly Gly Arg Ser Val Tyr Thr Glu Ala Tyr
103          145          150          155          160
104     Val Thr Ile Pro Val Gly Cys Thr Cys Val Pro Glu Pro Glu Lys Asp
105          165          170          175
106     Ala Asp Ser Ile Asn Ser Ser Ile Asp Lys Gln Gly Ala Lys Leu Leu
107          180          185          190
108     Leu Gly Pro Asn Asp Ala Pro Ala Gly Pro
109          195          200
110 <210> SEQ ID NO 3
111 <211> LENGTH: 187
112 <212> TYPE: PRT
113 <213> ORGANISM: Homo sapiens
114 <400> SEQUENCE: 3
115     Ala Gly Ala Pro Arg Ala Gly Arg Arg Pro Ala Arg Pro Arg Gly Cys
116         1          5          10          15
117     Ala Asp Arg Pro Glu Glu Leu Leu Glu Gln Leu Tyr Gly Arg Leu Ala
118         20          25          30
119     Ala Gly Val Leu Ser Ala Phe His His Thr Leu Gln Leu Gly Pro Arg
120         35          40          45
121     Glu Gln Ala Arg Asn Ala Ser Cys Pro Ala Gly Gly Arg Pro Ala Asp
122         50          55          60
123     Arg Arg Phe Arg Pro Pro Thr Asn Leu Arg Ser Val Ser Pro Trp Ala
124         65          70          75          80
125     Tyr Arg Ile Ser Tyr Asp Pro Ala Arg Tyr Pro Arg Tyr Leu Pro Glu
126         85          90          95
127     Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr Gly Leu Phe Gly Glu Glu
128         100          105          110
129     Asp Val Arg Phe Arg Ser Ala Pro Val Tyr Met Pro Thr Val Val Leu
130         115          120          125
131     Arg Arg Thr Pro Ala Cys Ala Gly Gly Arg Ser Val Tyr Thr Glu Ala
132         130          135          140
133     Tyr Val Thr Ile Pro Val Gly Cys Thr Cys Val Pro Glu Pro Glu Lys
134         145          150          155          160
135     Asp Ala Asp Ser Ile Asn Ser Ser Ile Asp Lys Gln Gly Ala Lys Leu
136         165          170          175
137     Leu Leu Gly Pro Asn Asp Ala Pro Ala Gly Pro
138         180          185
139 <210> SEQ ID NO 4
140 <211> LENGTH: 186
141 <212> TYPE: PRT
142 <213> ORGANISM: Homo sapiens
143 <400> SEQUENCE: 4
144     Gly Ala Pro Arg Ala Gly Arg Arg Pro Ala Arg Pro Arg Gly Cys Ala

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145      1      5      10      15
146  Asp Arg Pro Glu Glu Leu Leu Glu Gln Leu Tyr Gly Arg Leu Ala Ala
147      20      25      30
148  Gly Val Leu Ser Ala Phe His His Thr Leu Gln Leu Gly Pro Arg Glu
149      35      40      45
150  Gln Ala Arg Asn Ala Ser Cys Pro Ala Gly Gly Arg Pro Ala Asp Arg
151      50      55      60
152  Arg Phe Arg Pro Pro Thr Asn Leu Arg Ser Val Ser Pro Trp Ala Tyr
153      65      70      75      80
154  Arg Ile Ser Tyr Asp Pro Ala Arg Tyr Pro Arg Tyr Leu Pro Glu Ala
155      85      90      95
156  Tyr Cys Leu Cys Arg Gly Cys Leu Thr Gly Leu Phe Gly Glu Glu Asp
157      100      105      110
158  Val Arg Phe Arg Ser Ala Pro Val Tyr Met Pro Thr Val Val Leu Arg
159      115      120      125
160  Arg Thr Pro Ala Cys Ala Gly Gly Arg Ser Val Tyr Thr Glu Ala Tyr
161      130      135      140
162  Val Thr Ile Pro Val Gly Cys Thr Cys Val Pro Glu Pro Glu Lys Asp
163      145      150      155      160
164  Ala Asp Ser Ile Asn Ser Ser Ile Asp Lys Gln Gly Ala Lys Leu Leu
165      165      170      175
166  Leu Gly Pro Asn Asp Ala Pro Ala Gly Pro
167      180      185
168 <210> SEQ ID NO 5
169 <211> LENGTH: 185
170 <212> TYPE: PRT
171 <213> ORGANISM: Homo sapiens
172 <400> SEQUENCE: 5
173  Ala Pro Arg Ala Gly Arg Arg Pro Ala Arg Pro Arg Gly Cys Ala Asp
174      1      5      10      15
175  Arg Pro Glu Glu Leu Leu Glu Gln Leu Tyr Gly Arg Leu Ala Ala Gly
176      20      25      30
177  Val Leu Ser Ala Phe His His Thr Leu Gln Leu Gly Pro Arg Glu Gln
178      35      40      45
179  Ala Arg Asn Ala Ser Cys Pro Ala Gly Gly Arg Pro Ala Asp Arg Arg
180      50      55      60
181  Phe Arg Pro Pro Thr Asn Leu Arg Ser Val Ser Pro Trp Ala Tyr Arg
182      65      70      75      80
183  Ile Ser Tyr Asp Pro Ala Arg Tyr Pro Arg Tyr Leu Pro Glu Ala Tyr
184      85      90      95
185  Cys Leu Cys Arg Gly Cys Leu Thr Gly Leu Phe Gly Glu Glu Asp Val
186      100      105      110
187  Arg Phe Arg Ser Ala Pro Val Tyr Met Pro Thr Val Val Leu Arg Arg
188      115      120      125
189  Thr Pro Ala Cys Ala Gly Gly Arg Ser Val Tyr Thr Glu Ala Tyr Val
190      130      135      140
191  Thr Ile Pro Val Gly Cys Thr Cys Val Pro Glu Pro Glu Lys Asp Ala
192      145      150      155      160
193  Asp Ser Ile Asn Ser Ser Ile Asp Lys Gln Gly Ala Lys Leu Leu Leu
194      165      170      175

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195      Gly Pro Asn Asp Ala Pro Ala Gly Pro
196                      180                      185
197 <210> SEQ ID NO 6
198 <211> LENGTH: 23
199 <212> TYPE: DNA
200 <213> ORGANISM: Homo sapiens
201 <400> SEQUENCE: 6
202      ccgggtcgtgta ggagattctg tag                                23
203 <210> SEQ ID NO 7
204 <211> LENGTH: 22
205 <212> TYPE: DNA
206 <213> ORGANISM: Homo sapiens
207 <400> SEQUENCE: 7
208      gcgtgctcag tgccttccac ca                                22
209 <210> SEQ ID NO 8
210 <211> LENGTH: 1221
211 <212> TYPE: DNA
212 <213> ORGANISM: Mus musculus
213 <220> FEATURE:
214 <221> NAME/KEY: CDS
215 <222> LOCATION: (79)...(693)
216 <400> SEQUENCE: 8
217      ggggtgtcgcc cttatttact tcgcagaaga gccttcagcc cccctcctaa caagtctgga    60
218      aagcatcacg gcgacgcg atg ttg ggg aca ctg gtc tgg atg ctc gcg gtc    111
219                      Met Leu Gly Thr Leu Val Trp Met Leu Ala Val
220                      1                      5                      10
221      ggc ttc ctg ctg gca ctg gcg ccg ggc cgc gcg ggc ggc ctg agg    159
222      Gly Phe Leu Leu Ala Leu Ala Pro Gly Arg Ala Ala Gly Ala Leu Arg
223                      15                      20                      25
224      acc ggg agg cgc ccg gcg ccg ccg gac tgc gcg gac ccg ccg gag    207
225      Thr Gly Arg Arg Pro Ala Arg Pro Arg Asp Cys Ala Asp Arg Pro Glu
226                      30                      35                      40
227      gag ctc ctg gag cag ctg tac ggg ccg ctg gcg gcc ggc gtg ctc agc    255
228      Glu Leu Leu Glu Gln Leu Tyr Gly Arg Leu Ala Ala Gly Val Leu Ser
229                      45                      50                      55
230      gcc ttc cac cac acg ctg cag ctc ggg ccg cgc gag cag gcg cgc aat    303
231      Ala Phe His His Thr Leu Gln Leu Gly Pro Arg Glu Gln Ala Arg Asn
232                      60                      65                      70                      75
233      gcc agc tgc ccg gcc ggg ggc agg gcc gcc gac cgc cgc ttc ccg cca    351
234      Ala Ser Cys Pro Ala Gly Gly Arg Ala Ala Asp Arg Arg Phe Arg Pro
235                      80                      85                      90
236      ccc acc aac ctg cgc agc gtg tcg ccc tgg gcg tac agg att tcc tac    399
237      Pro Thr Asn Leu Arg Ser Val Ser Pro Trp Ala Tyr Arg Ile Ser Tyr
238                      95                      100                      105
239      gac cct gct cgc ttt ccg agg tac ctg ccc gaa gcc tac tgc ctg tgc    447
240      Asp Pro Ala Arg Phe Pro Arg Tyr Leu Pro Glu Ala Tyr Cys Leu Cys
241                      110                      115                      120
242      cga ggc tgc ctg acc ggg ctc tac ggg gag gag gac ttc cgc ttt cgc    495
243      Arg Gly Cys Leu Thr Gly Leu Tyr Gly Glu Glu Asp Phe Arg Phe Arg
244                      125                      130                      135

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VERIFICATION SUMMARY
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| Line | ? Error/Warning | Original Text |
|------|--|---|
| 425 | W Line data has been corrected | Leu Gly Pro Asn Asp Ala Pro Ala Gly Pro |
| 426 | W Invalid/Missing Amino Acid Numbering | 200 205 |